J. Roark

#16

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RAW SEQUENCE LISTING                    DATE: 05/24/2002
PATENT APPLICATION:  US/09/671,658A     TIME: 09:44:30

Input Set : N:\Crf3\RULE60\09671658A.RAW
Output Set: N:\CRF3\05242002\I671658A.raw

              SEQUENCE LISTING
 3 (1) GENERAL INFORMATION:
 5       (i) APPLICANT: Gorman, Daniel M.
 6                      Mattson, Jeanine D.
 8      (ii) TITLE OF INVENTION: Mammalian Cell Surface Antigens; Related
 9                               Reagents
11     (iii) NUMBER OF SEQUENCES: 2
13      (iv) CORRESPONDENCE ADDRESS:
14           (A) ADDRESSEE: DNAX Research Institute
15           (B) STREET: 901 California Avenue
16           (C) CITY: Palo Alto
17           (D) STATE: California
18           (E) COUNTRY: USA
19           (F) ZIP: 94304-1104
21       (v) COMPUTER READABLE FORM:
22           (A) MEDIUM TYPE: Floppy disk
23           (B) COMPUTER: IBM PC compatible
24           (C) OPERATING SYSTEM: PC-DOS/MS-DOS
25           (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
27      (vi) CURRENT APPLICATION DATA:
28           (A) APPLICATION NUMBER: US/09/671,658A
29           (B) FILING DATE: 27-Sep-2000
30           (C) CLASSIFICATION:
32     (vii) PRIOR APPLICATION DATA:
34           (A) APPLICATION NUMBER: US/08/989,362
35           (B) FILING DATE: 12-DEC-1997
37           (A) APPLICATION NUMBER: US 60/032,846
38           (B) FILING DATE: 13-DEC-1996
40    (viii) ATTORNEY/AGENT INFORMATION:
41           (A) NAME: Ching, Edwin P.
42           (B) REGISTRATION NUMBER: 34,090
43           (C) REFERENCE/DOCKET NUMBER: DX0686
45      (ix) TELECOMMUNICATION INFORMATION:
46           (A) TELEPHONE: (650)852-9196
47           (B) TELEFAX: (650)496-1204
50 (2) INFORMATION FOR SEQ ID NO: 1:
52       (i) SEQUENCE CHARACTERISTICS:
53           (A) LENGTH: 2191 base pairs
54           (B) TYPE: nucleic acid
55           (C) STRANDEDNESS: single
56           (D) TOPOLOGY: linear
58      (ii) MOLECULE TYPE: cDNA
61      (ix) FEATURE:
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C--> 28
C--> 29

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62          (A) NAME/KEY: CDS
63          (B) LOCATION: 125..1072
66     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
68 GCCAGGACCT CTGTGAACCG GTCGGGGCGG GGGCCGCCTG GCCGGGAGTC TGCTCGGCGG        60
70 TGGGTGGCCG AGGAAGGGAG AGAACGATCG CGGAGCAGGG CGCCCGAACT CCGGGCGCCG       120
72 CGCC ATG CGC CGG GCC AGC CGA GAC TAC GGC AAG TAC CTG CGC AGC TCG       169
73      Met Arg Arg Ala Ser Arg Asp Tyr Gly Lys Tyr Leu Arg Ser Ser
74       1               5                  10                  15
76 GAG GAG ATG GGC AGC GGC CCC GGC GTC CCA CAC GAG GGT CCG CTG CAC       217
77 Glu Glu Met Gly Ser Gly Pro Gly Val Pro His Glu Gly Pro Leu His
78              20                  25                  30
80 CCC GCG CCT TCT GCA CCG GCT CCG GCG CCG CCA CCC GCC GCC TCC CGC       265
81 Pro Ala Pro Ser Ala Pro Ala Pro Ala Pro Pro Ala Ala Ser Arg
82              35                  40                  45
84 TCC ATG TTC CTG GCC CTC CTG GGG CTG GGA CTG GGC CAG GTG GTC TGC       313
85 Ser Met Phe Leu Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys
86          50                  55                  60
88 AGC ATC GCT CTG TTC CTG TAC TTT CGA GCG CAG ATG GAT CCT AAC AGA       361
89 Ser Ile Ala Leu Phe Leu Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg
90       65                  70                  75
92 ATA TCA GAA GAC AGC ACT CAC TGC TTT TAT AGA ATC CTG AGA CTC CAT       409
93 Ile Ser Glu Asp Ser Thr His Cys Phe Tyr Arg Ile Leu Arg Leu His
94 80                  85                  90                  95
96 GAA AAC GCA GGT TTG CAG GAC TCG ACT CTG GAG AGT GAA GAC ACA CTA       457
97 Glu Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu Ser Glu Asp Thr Leu
98              100                 105                 110
100 CCT GAC TCC TGC AGG AGG ATG AAA CAA GCC TTT CAG GGG GCC GTG CAG      505
101 Pro Asp Ser Cys Arg Arg Met Lys Gln Ala Phe Gln Gly Ala Val Gln
102              115                 120                 125
104 AAG GAA CTG CAA CAC ATT GTG GGG CCA CAG CGC TTC TCA GGA GCT CCA      553
105 Lys Glu Leu Gln His Ile Val Gly Pro Gln Arg Phe Ser Gly Ala Pro
106          130                 135                 140
108 GCT ATG ATG GAA GGC TCA TGG TTG GAT GTG GCC CAG CGA GGC AAG CCT      601
109 Ala Met Met Glu Gly Ser Trp Leu Asp Val Ala Gln Arg Gly Lys Pro
110      145                 150                 155
112 GAG GCC CAG CCA TTT GCA CAC CTC ACC ATC AAT GCT GCC AGC ATC CCA      649
113 Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro
114 160                 165                 170                 175
116 TCG GGT TCC CAT AAA GTC ACT CTG TCC TCT TGG TAC CAC GAT CGA GGC      697
117 Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly
118              180                 185                 190
120 TGG GCC AAG ATC TCT AAC ATG ACG TTA AGC AAC GGA AAA CTA AGG GTT      745
121 Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val
122              195                 200                 205
124 AAC CAA GAT GGC TTC TAT TAC CTG TAC GCC AAC ATT TGC TTT CGG CAT      793
125 Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His
126              210                 215                 220
128 CAT GAA ACA TCG GGA AGC GTA CCT ACA GAC TAT CTT CAG CTG ATG GTG      841
129 His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val
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130     225                     230                     235
132 TAT GTC GTT AAA ACC AGC ATC AAA ATC CCA AGT TCT CAT AAC CTG ATG     889
133 Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met
134 240                 245                 250                 255
136 AAA GGA GGG AGC ACG AAA AAC TGG TCG GGC AAT TCT GAA TTC CAC TTT     937
137 Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe
138                 260                 265                 270
140 TAT TCC ATA AAT GTT GGG GGA TTT TTC AAG CTC CGA GCT GGT GAA GAA     985
141 Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu
142                 275                 280                 285
144 ATT AGC ATT CAG GTG TCC AAC CCT TCC CTG CTG GAT CCG GAT CAA GAT    1033
145 Ile Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp
146         290                 295                 300
148 GCG ACG TAC TTT GGG GCT TTC AAA GTT CAG GAC ATA GAC TGAGACTCAT    1082
149 Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp
150     305                 310                 315
152 TTCGTGGAAC ATTAGCATGG ATGTCCTAGA TGTTTGGAAA CTTCTTAAAA AATGGATGAT    1142
154 GTCTATACAT GTGTAAGACT ACTAAGAGAC ATGGCCCACG GTGTATGAAA CTCACAGCCC    1202
156 TCTCTCTTGA GCCTGTACAG GTTGTGTATA TGTAAAGTCC ATAGGTGATG TTAGATTCAT    1262
158 GGTGATTACA CAACGGTTTT ACAATTTTGT AATGATTTCC TAAGAATTGA ACCAGATTGG    1322
160 GAGAGGTATT CCGATGCTTA TGAAAAACTT ACACGTGAGC TATGGAAGGG GGTCACAGTC    1382
162 TCTGGGTCTA ACCCCTGGAC ATGTGCCACT GAGAACCTTG AAATTAAGAA GATGCCATGT    1442
164 CATTGCAAAG AAATGATAGT GTGAAGGGTT AAGTTCTTTT GAATTGTTAC ATTGCGCTGG    1502
166 GACCTGCAAA TAAGTTCTTT TTTTCTAATG AGGAGAGAAA AATATATGTA TTTTTATATA    1562
168 ATGTCTAAAG TTATATTTCA GGTGTAATGT TTTCTGTGCA AAGTTTTGTA AATTATATTT    1622
170 GTGCTATAGT ATTTGATTCA AAATATTTAA AAATGTCTCA CTGTTGACAT ATTTAATGTT    1682
172 TTAAATGTAC AGATGTATTT AACTGGTGCA CTTTGTAATT CCCCTGAAGG TACTCGTAGC    1742
174 TAAGGGGGCA GAATACTGTT TCTGGTGACC ACATGTAGTT TATTTCTTTA TTCTTTTTAA    1802
176 CTTAATAGAG TCTTCAGACT TGTCAAAACT ATGCAAGCAA AATAAATAAA TAAAAATAAA    1862
178 ATGAATATCT TGAATAATAA GTAGGATGTT GGTCACCAGG TGCCTTTCAA ATTTAGAAGC    1922
180 TAATTGACTT TAGGAGCTGA CATAGCCAAA AAGGATACAT AATAGGCTAC TGAAAATCTG    1982
182 TCAGGAGTAT TTATGCAATT ATTGAACAGG TGTCTTTTTT TACAAGAGCT ACAAATTGTA    2042
184 AATTTTGTTT CTTTTTTTTC CCATAGAAAA TGTACTATAG TTTATCAGCC AAAAAACAAT    2102
186 CCACTTTTTA ATTTAGTGAA AGTTATTTTA TTATACTGTA CAATAAAAGC ATTGTTTCTG    2162
188 AATGGCATTT TTTGGTACTT AAAAATGGC                                     2191
191 (2) INFORMATION FOR SEQ ID NO: 2:
193     (i) SEQUENCE CHARACTERISTICS:
194         (A) LENGTH: 316 amino acids
195         (B) TYPE: amino acid
196         (D) TOPOLOGY: linear
198     (ii) MOLECULE TYPE: protein
200     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
202 Met Arg Arg Ala Ser Arg Asp Tyr Gly Lys Tyr Leu Arg Ser Ser Glu
203   1               5                   10                  15
205 Glu Met Gly Ser Gly Pro Gly Val Pro His Glu Gly Pro Leu His Pro
206             20                  25                  30
208 Ala Pro Ser Ala Pro Ala Pro Ala Pro Pro Ala Ala Ser Arg Ser
209         35                  40                  45
211 Met Phe Leu Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser
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212      50                    55                   60
214 Ile Ala Leu Phe Leu Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile
215  65                    70                   75                   80
217 Ser Glu Asp Ser Thr His Cys Phe Tyr Arg Ile Leu Arg Leu His Glu
218                    85                   90                   95
220 Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro
221                   100                  105                  110
223 Asp Ser Cys Arg Arg Met Lys Gln Ala Phe Gln Gly Ala Val Gln Lys
224            115                  120                  125
226 Glu Leu Gln His Ile Val Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala
227        130                  135                  140
229 Met Met Glu Gly Ser Trp Leu Asp Val Ala Gln Arg Gly Lys Pro Glu
230 145                  150                  155                  160
232 Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser
233                   165                  170                  175
235 Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly Trp
236            180                  185                  190
238 Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val Asn
239            195                  200                  205
241 Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His
242        210                  215                  220
244 Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr
245 225                  230                  235                  240
247 Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met Lys
248            245                  250                  255
250 Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr
251            260                  265                  270
253 Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile
254        275                  280                  285
256 Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala
257        290                  295                  300
259 Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp
260 305                  310                  315
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VERIFICATION SUMMARY   DATE: 05/24/2002
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L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]